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<120> Novel Methods for Therapeutic Vaccination

<130> 3631-0109P

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<160> 41

<170> PatentIn Ver. 3.0

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Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
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ttt ctc ctc ggc ttc ctc ttc ggg tgg ttt ata aaa tcc tcc aat gaa
Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

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Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile	
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caa tcc cag tgg aaa gaa ttt ggc ctg gat tct gtt gag cta gca cat	336
Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His	
100 105 110	
tat gat gtc ctg ttg tcc tac cca aat aag act cat ccc aac tac atc	384
Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile	
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Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe	
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Glu Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro	
145 150 155 160	
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Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met	
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Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val	
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Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly	
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Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys	
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Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser	
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625 630 635 640	
gaa att gct tcc aag ttc agt gag aga ctc cag gac ttt gac aaa agc	1968
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645 650 655	

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His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser		
690 695 700		
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Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp		
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Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe		
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Glu Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro		
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Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met		
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 245 250 255
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 275 280 285
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 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
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 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
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 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
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 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
 370 375 380
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 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
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 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
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Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys	
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Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu	
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Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr	
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Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	
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										125					135	
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Asn Gln Leu Ala Leu Thr	Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys		
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His Pro Cys Ser Pro Met	Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser		
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tct gag gat tgt cag	agc ctg acg cgc act gtc tgt gcc ggt ggc tgt	672	
Ser Glu Asp Cys Gln	Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys		
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205	210	215	
gct gcc ggc tgc acg	ggc ccc aag cac tct gac tgc ctg gcc tgc ctc	768	
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tat aca ttc ggc gcc	agc tgt gtg act gcc tgt ccc tac aac tac ctt	912	
Tyr Thr Phe Gly Ala	Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu		
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365	370	375	
gag act ctg gaa gag	atc aca ggt tac cta tac atc tca gca tgg ccg	1248	
Glu Thr Leu Glu Ile	Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro		
380	385	390	
gac agc ctg cct gac	ctc agc gtc ttc cag aac ctg caa gta atc cgg	1296	
Asp Ser Leu Pro Asp	Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg		
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Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys			
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Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys			
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Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp			
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Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys			
605	610	615	
ggc tgc ccc gcc gag cag aga gcc agc cct ctg acg tcc atc gtc tct			1968
Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser			
620	625	630	
gcg gtg gtt ggc att ctg ctg gtc gtg gtc ttg ggg gtg gtc ttt ggg			2016
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly			
635	640	645	
atc ctc atc aag cga cgg cag cag aag atc cgg aag tac acg atg cgg			2064
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg			
650	655	660	665
aga ctg ctg cag gaa acg gag ctg gtg gag ccg ctg aca cct agc gga			2112
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly			
670	675	680	
gcg atg ccc aac cag gcg cag atg cgg atc ctg aaa gag acg gag ctg			2160
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu			
685	690	695	
agg aag gtg aag gtg ctt gga tct ggc gct ttt ggc aca gtc tac aag			2208
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys			
700	705	710	
ggc atc tgg atc cct gat ggg gag aat gtg aaa att cca gtg gcc atc			2256
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile			
715	720	725	
aaa gtg ttg agg gaa aac aca tcc ccc aaa gcc aac aaa gaa atc tta			2304
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu			
730	735	740	745
gac gaa gca tac gtg atg gct ggt gtg ggc tcc cca tat gtc tcc cgc			2352
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg			
750	755	760	
ctt ctg ggc atc tgc ctg aca tcc acg gtg cag ctg gtg aca cag ctt			2400

Leu	Leu	Gly	Ile	Cys	Leu	Thr	Ser	Thr	Val	Gln	Leu	Val	Thr	Gln	Leu			
765								770					775					
atg	ccc	tat	ggc	tgc	ctc	tta	gac	cat	gtc	cg	gaa	aac	cgc	gga	cgc			
Met	Pro	Tyr	Gly	Cys	Leu	Leu	Asp	His	Val	Arg	Glu	Asn	Arg	Gly	Arg			
									785				790					
ctg	ggc	tcc	cag	gac	ctg	ctg	aac	tgg	tgt	atg	cag	att	gcc	aag	ggg			
Leu	Gly	Ser	Gln	Asp	Leu	Leu	Asn	Trp	Cys	Met	Gln	Ile	Ala	Lys	Gly			
									795	800			805					
atg	agc	tac	ctg	gag	gat	gtg	cg	ctc	gta	cac	agg	gac	ttg	gcc	gct			
Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu	Ala	Ala			
									810	815			820		825			
cg	gg	aac	gt	ct	gt	gt	aag	agt	ccc	aac	cat	gtc	aaa	att	aca	gac	ttc	
Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr	Asp	Phe			
									830		835			840				
ggg	ctg	gct	cg	ctg	gac	att	gac	gag	aca	gag	tac	cat	gca	gat		2640		
Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His	Ala	Asp			
									845	850			855					
ggg	ggc	aag	gt	cc	atc	aag	tgg	atg	g	ctg	gag	tcc	att	ctc	cg		2688	
Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile	Leu	Arg			
									860	865			870					
cg	cg	t	tc	acc	cac	cag	agt	gat	gt	tgg	agt	tat	gg	gt	act	gt		2736
Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr	Val			
									875	880			885					
tgg	gag	ctg	atg	act	ttt	ggg	gcc	aaa	cct	tac	gat	ggg	atc	cca	gcc		2784	
Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Ala			
									890	895			900		905			
cg	gag	atc	cct	gac	ctg	ctg	gaa	aag	ggg	gag	cg	ctg	ccc	cag	ccc		2832	
Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro	Gln	Pro			
									910		915			920				
ccc	atc	tgc	acc	att	gat	gtc	tac	atg	atc	atg	gtc	aaa	tgt	tgg	atg		2880	
Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met			
									925	930			935					
att	gac	tct	gaa	tgt	cg	cca	aga	ttc	cg	gag	ttg	gt	tct	gaa	ttc		2928	
Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe			
									940	945			950					
tcc	cgc	atg	ggc	agg	gac	ccc	cag	cg	ttt	gt	gtc	atc	cag	aat	gag		2976	
Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu			
									955	960			965					
gac	ttg	ggc	cc	g	cc	agt	ccc	ttg	gac	agc	acc	ttc	tac	cg	tca	ctg		3024
Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg	Ser	Leu			
									970	975			980		985			
ctg	gag	gac	gat	gac	atg	ggg	gac	ctg	gt	gt	gat	gct	gag	gag	tat	ctg		3072
Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu	Tyr	Leu			
									990		995			1000				
gta	ccc	cag	cag	ggc	t	ttc	t	tgc	cca	gac	cct	gcc	ccg	ggc	gct	ggg		3120
Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly			
									1005	1010			1015					
ggc	atg	gt	cac	cac	agg	cac	cg	ac	tca	tct	acc	agg	agt	ggc	gg		3168	
Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser	Gly	Gly			
									1020	1025			1030					
ggg	gac	ctg	aca	cta	ggg	ctg	gag	ccc	tct	gaa	gag	gag	gcc	ccc	agg		3216	
Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala	Pro	Arg			
									1035	1040			1045					
tct	cca	ctg	gca	ccc	tcc	gaa	ggg	gct	ggc	tcc	gat	gta	ttt	gat	ggt		3264	
Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly			
									1050	1055			1060		1065			

gac ctg gga atg ggg gca gcc aag ggg ctg caa agc ctc ccc aca cat		3312	
Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His			
1070	1075	1080	
gac ccc agc cct cta cag cgg tac agt gag gac ccc aca gta ccc ctg		3360	
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu			
1085	1090	1095	
ccc tct gag act gat ggc tac gtt gcc ccc ctg acc tgc agc ccc cag		3408	
Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln			
1100	1105	1110	
cct gaa tat gtg aac cag cca gat gtt cgg ccc cag ccc cct tcg ccc		3456	
Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro			
1115	1120	1125	
cga gag ggc cct ctg cct gct gcc cga cct gct ggt gcc act ctg gaa		3504	
Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu			
1130	1135	1140	1145
agg gcc aag act ctc tcc cca ggg aag aat ggg gtc gtc aaa gac gtt		3552	
Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val			
1150	1155	1160	
ttt gcc ttt ggg ggt gcc gtg gag aac ccc gag tac ttg aca ccc cag		3600	
Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln			
1165	1170	1175	
gga gga gct gcc cct cag ccc cac cct cct gcc ttc agc cca gcc		3648	
Gly Gly Ala Ala Pro Gln Pro His Pro Pro Ala Phe Ser Pro Ala			
1180	1185	1190	
ttc gac aac ctc tat tac tgg gac cag gac cca cca gag cgg ggg gct		3696	
Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala			
1195	1200	1205	
cca ccc agc acc ttc aaa ggg aca cct acg gca gag aac cca gag tac		3744	
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr			
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ctg ggt ctg gac gtg cca gtg tga		3768	
Leu Gly Leu Asp Val Pro Val			
1230			

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<213> Homo sapiens

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Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys			
-5	-1	1	
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His			
10	15	20	25
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr			
30	35	40	
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val			
45	50	55	
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu			
60	65	70	
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr			
75	80	85	
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro			
90	95	100	105

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
 110 115 120
 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
 125 130 135
 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
 140 145 150
 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
 155 160 165
 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
 170 175 180 185
 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 190 195 200
 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 205 210 215
 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 220 225 230
 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
 235 240 245
 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
 250 255 260 265
 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
 270 275 280
 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
 285 290 295
 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
 300 305 310
 Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
 315 320 325
 Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
 330 335 340 345
 Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
 350 355 360
 Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
 365 370 375
 Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
 380 385 390
 Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
 395 400 405
 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
 410 415 420 425
 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
 430 435 440
 Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
 445 450 455
 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
 460 465 470
 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
 475 480 485
 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
 490 495 500 505
 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
 510 515 520
 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
 525 530 535
 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
 540 545 550
 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp

555	560	565
Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu		
570 575	580	585
Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln		
590	595	600
Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys		
605	610	615
Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser		
620	625	630
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly		
635	640	645
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg		
650 655	660	665
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly		
670	675	680
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu		
685	690	695
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys		
700	705	710
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile		
715	720	725
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu		
730 735	740	745
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg		
750	755	760
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu		
765	770	775
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg		
780	785	790
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly		
795	800	805
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala		
810 815	820	825
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe		
830	835	840
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp		
845	850	855
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg		
860	865	870
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val		
875	880	885
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala		
890	895	900
905		
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro		
910	915	920
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met		
925	930	935
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe		
940	945	950
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu		
955	960	965
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu		
970	975	980
985		
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu		
990	995	1000
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly		
1005	1010	1015

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
 1020 1025 1030
 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Ala Pro Arg
 1035 1040 1045
 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
 1050 1055 1060 1065
 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
 1070 1075 1080
 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
 1085 1090 1095
 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
 1100 1105 1110
 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
 1115 1120 1125
 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 1130 1135 1140 1145
 Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
 1150 1155 1160
 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 1165 1170 1175
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
 1180 1185 1190
 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
 1195 1200 1205
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 1210 1215 1220 1225
 Leu Gly Leu Asp Val Pro Val
 1230

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 gtt ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30
 aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144
 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45
 cgc ctc atc cgg acc tac cag ctc tac agc cgc acc agc ggg aag cac 192
 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60
 gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gaa gac gga 240
 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80
 gac ccc ttc gcg aag ctc att gtg gag acc gat act ttt gga agc aga 288
 Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg

85	90	95	
gtc cga gtt cgc ggc gca gag aca ggt ctc tac atc tgc atg aac aag			336
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys			
100	105	110	
aag ggg aag cta att gcc aag agc aac ggc aaa ggc aag gac tgc gta			384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val			
115	120	125	
ttc aca gag atc gtg ctg gag aac aac tac acg gcg ctg cag aac gcc			432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala			
130	135	140	
aag tac gag ggc tgg tac atg gcc ttt acc cgc aag ggc cgg ccc cgc			480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg			
145	150	155	160
aag ggc tcc aag acg cgc cag cat cag cgc gag gtg cac ttc atg aag			528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys			
165	170	175	
cgc ctg ccg cgg ggc cac cac acc acc gag cag acg ctg cgc ttc gag			576
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu			
180	185	190	
ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg			624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg			
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act tgg gcc ccg gag ccc cga tag			648
Thr Trp Ala Pro Glu Pro Arg			
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Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu			
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Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe			
20	25	30	
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg			
35	40	45	
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His			
50	55	60	
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly			
65	70	75	80
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg			
85	90	95	
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys			
100	105	110	
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val			
115	120	125	
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala			
130	135	140	
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg			
145	150	155	160
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys			
165	170	175	
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu			
180	185	190	

Phe	Leu	Asn	Tyr	Pro	Fro	Phe	Thr	Arg	Ser	Leu	Arg	Gly	Ser	Gln	Arg
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Thr	Trp	Ala	Pro	Glu	Pro	Arg									
210				215											

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Met	Trp	Asn	Ala	Leu	Gln	Asp	Arg	Asp	Ser	Ala	Glu	Val	Leu	Gly	His
1									10					15	
cgc	cag	cgc	tgg	ctc	cgt	gtt	ggg	aca	ctg	gtg	ctg	gct	tta	acc	gga
Arg	Gln	Arg	Trp	Leu	Arg	Val	Gly	Thr	Leu	Val	Leu	Ala	Leu	Thr	Gly
									20		25			30	
acc	ttc	ctc	att	ggc	ttc	ctc	ttt	ggg	tgg	ttt	ata	aaa	cct	tcc	aat
Thr	Phe	Leu	Ile	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Pro	Ser	Asn
										35	40		45		
gaa	gct	act	ggt	aat	gtt	tcc	cat	tct	ggc	atg	aag	aag	gag	ttt	ttg
Glu	Ala	Thr	Gly	Asn	Val	Ser	His	Ser	Gly	Met	Lys	Lys	Glu	Phe	Leu
										50	55		60		
cat	gaa	ttg	aag	gct	gag	aac	atc	aaa	aaa	ttt	tta	tac	aat	ttc	aca
His	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr	Asn	Phe	Thr
										65	70		75		80
cgg	aca	cca	cac	ttg	gca	gga	aca	caa	aat	aat	ttt	gag	ctt	gca	aag
Arg	Thr	Pro	His	Leu	Ala	Gly	Thr	Gln	Asn	Asn	Phe	Glu	Leu	Ala	Lys
										85	90		95		
caa	att	cat	gac	cag	tgg	aaa	gaa	ttt	ggc	ctg	gat	tgg	gtt	gag	tta
Gln	Ile	His	Asp	Gln	Trp	Lys	Glu	Phe	Gly	Leu	Asp	Leu	Val	Glu	Leu
										100	105		110		
tcc	cat	tac	gat	gtc	ttg	ctg	tcc	tat	cca	aat	aaa	act	cat	cct	aac
Ser	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	Asn	Lys	Thr	His	Pro	Asn
										115	120		125		
tat	atc	tca	ata	att	aat	gaa	gat	ggg	aat	gag	att	ttc	aaa	aca	tca
Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	Glu	Ile	Phe	Lys	Thr	Ser
										130	135		140		
tta	tct	gaa	cag	cca	ccc	cca	gga	tat	gag	aat	ata	tca	gat	gtt	gtg
Leu	Ser	Glu	Gln	Pro	Pro	Gly	Tyr	Glu	Asn	Ile	Ser	Asp	Val	Val	
										145	150		155		160
cca	cca	tac	agt	gcc	ttc	tct	cca	caa	ggg	aca	cca	gag	ggg	gtt	gat
Pro	Pro	Tyr	Ser	Ala	Phe	Ser	Pro	Gln	Gly	Thr	Pro	Glu	Gly	Asp	Leu
										165	170		175		
gtg	tat	gtc	aac	tat	gca	cga	act	gaa	gac	ttc	ttt	aaa	ctg	gaa	cg
Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg
										180	185		190		
gaa	atg	aag	atc	agt	tgt	tct	ggg	aag	att	gtg	att	gcc	aga	tat	ggg
Glu	Met	Lys	Ile	Ser	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly
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Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn	Aia	Gln	Leu	Ala	Gly	Ala	
210						215					220					
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Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Val	Pro	Ala	
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gtg	aag	tcc	tat	cca	gat	ggc	tgg	aac	ctc	cct	gga	ggt	ggt	gtc	caa	763
Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Val	Gln		
						245				250			255			
cgt	gga	aat	gtc	tta	aat	ctt	aat	ggt	gca	ggt	gac	ccg	ctc	aca	cca	816
Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
						260			265			270				
ggt	tac	cca	gca	aat	gaa	cat	gct	tat	agg	cat	gag	ttg	aca	aac	gct	864
Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg	His	Glu	Leu	Thr	Asn	Ala	
						275			280			285				
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Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Asp	Asp	Ala	
						290			295			300				
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Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro	Ala	Pro	Pro	Asp	Ser	Ser	
						305			310			315			320	
tgg	aag	gga	gga	tta	aaa	gtg	cct	tac	aac	gtg	gga	cct	ggc	ttt	gct	1008
Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Ala	
						325			330			335				
gga	aac	ttt	tca	aca	caa	aag	gtc	aag	atg	cat	att	cac	tct	tac	act	1056
Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Tyr	Thr	
						340			345			350				
aaa	gtg	aca	aga	atc	tat	aat	gtc	att	ggc	acc	ctc	aaa	gga	gct	ctg	1104
Lys	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Lys	Gly	Ala	Leu	
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gaa	cca	gac	aga	tat	gtt	att	ctt	gga	ggt	cac	cga	gac	gct	tgg	gta	1152
Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ala	Trp	Val	
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Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile	
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gtg	cgg	agc	ttt	gga	acc	ctg	aag	aag	aaa	gga	cgg	agg	cct	aga	agg	1248
Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Gly	Arg	Arg	Pro	Arg	Arg		
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aca	att	ttg	ttt	gca	agc	tgg	gat	gca	gaa	gaa	ttt	ggc	ctt	ctt	ggt	1296
Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	
						420			425			430				
tct	act	gag	tgg	gca	gag	gaa	cat	tca	aga	ctc	cta	caa	gag	cga	ggt	1344
Ser	Thr	Glu	Trp	Ala	Glu	Glu	His	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	
						435			440			445				
gtg	gct	tat	att	aat	gct	gat	tct	tcc	ata	gaa	gga	aat	tac	act	cta	1392
Val	Ala	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	
						450			455			460				
aga	gtt	gat	tgc	aca	cca	ctg	atg	tac	agc	tta	gtg	tac	aac	cta	aca	1440
Arg	Val	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	Tyr	Asn	Leu	Thr	
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Lys	Glu	Leu	Gln	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	
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gac	agc	tgg	aaa	gaa	aag	agt	cct	tca	cct	gag	ttc	att	gga	atg	ccc	1536
Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro	
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aga	att	agc	aag	ctg	ggg	tct	ggc	aat	gat	ttt	gaa	gtg	ttc	ttc	caa	1584

Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln			
515	520	525	
aga ctt gga att gct tca ggc aga gcc cga tat act aaa aat tgg aaa			1632
Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Lys			
530	535	540	
act aac aas gtc agc agc tat cct ctc tat cac agt gtc tat gaa aca			1680
Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr			
545	550	555	560
tat gag ctg gta gta aaa ttt tat gac cca aca ttt aaa tac cac ctc			1728
Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro Thr Phe Lys Tyr His Leu			
565	570	575	
act gtg gcc cag gtt cga ggaa gcg atg gta ttt gaa ctt gcc aat tct			1776
Thr Val Ala Gln Val Arg Gly Ala Met Val Phe Glu Leu Ala Asn Ser			
580	585	590	
ata gtg ctt ccc ttt gac tgc caa agt tat gct gta gct ctg aag aag			1824
Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr Ala Val Ala Leu Lys Lys			
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tat gct gac act atc tac aat att tca atg aaa cat cca caa gaa atg			1872
Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met			
610	615	620	
aag gct tac atg ata tca ttt gat tca ctg ttt tct gca gtc aat aat			1920
Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu Phe Ser Ala Val Asn Asn			
625	630	635	640
ttt aca gat gtt gca tct aag ttc aat cag aga ctg caa gag tta gac			1968
Phe Thr Asp Val Ala Ser Lys Phe Asn Gln Arg Leu Gln Glu Leu Asp			
645	650	655	
aaa agc aac ccc ata tta ctg aga att atg aat gac cag ctg atg tat			2016
Lys Ser Asn Pro Ile Leu Leu Arg Ile Met Asn Asp Gln Leu Met Tyr			
660	665	670	
ctg gaa cgt gca ttc att gat cct tta ggc tta cca gga agg cct ttc			2064
Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Gly Arg Pro Phe			
675	680	685	
tac agg cat acc atc tat gct cca agc agc cac aac aag tat gca gga			2112
Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly			
690	695	700	
gaa tca ttc cct ggg att tat gat gcc ctt ttt gat ata agt agc aaa			2160
Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Ser Ser Lys			
705	710	715	720
gtc aat gct tct aag gcc tgg aac gaa gtg aag aga cag att tct att			2208
Val Asn Ala Ser Lys Ala Trp Asn Glu Val Lys Arg Gln Ile Ser Ile			
725	730	735	
gca acc ttt aca gtg caa gct gca gca gag act ctg agg gaa gta gct			2256
Ala Thr Phe Thr Val Gln Ala Ala Glu Thr Leu Arg Glu Val Ala			
740	745	750	

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20 25 30
Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn

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Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys	Glu Phe Leu	
50	55	60
His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr	Asn Phe Thr	
65	70	75
Arg Thr Pro His Leu Ala Gly Thr Gln Asn Asn Phe Glu	Leu Ala Lys	
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Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu	Val Glu Leu	
100	105	110
Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr	His Pro Asn	
115	120	125
Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe	Lys Thr Ser	
130	135	140
Leu Ser Glu Gln Pro Pro Gly Tyr Glu Asn Ile Ser Asp	Val Val	
145	150	155
160		
Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Glu	Gly Asp Leu	
165	170	175
Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys	Leu Glu Arg	
180	185	190
Glu Met Lys Ile Ser Cys Ser Gly Lys Ile Val Ile Ala	Arg Tyr Gly	
195	200	205
Lys Val Phe Arg Gly Asn Met Val Lys Asn Ala Gln	Leu Ala Gly Ala	
210	215	220
Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe	Val Pro Ala	
225	230	235
240		
Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly	Val Gln	
245	250	255
Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp Pro	Leu Thr Pro	
260	265	270
Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg His Glu Leu	Thr Asn Ala	
275	280	285
Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr	Asp Asp Ala	
290	295	300
Gln Lys Leu Leu Glu His Met Gly Gly Pro Ala Pro Pro	Asp Ser Ser	
305	310	315
320		
Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn Val Gly Pro	Gly Phe Ala	
325	330	335
Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile His	Ser Tyr Thr	
340	345	350
Lys Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Lys	Gly Ala Leu	
355	360	365
Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp	Ala Trp Val	
370	375	380
Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val	His Glu Ile	
385	390	395
400		
Val Arg Ser Phe Gly Thr Leu Lys Lys Gly Arg Arg Pro	Arg Arg	
405	410	415
Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly	Leu Leu Gly	
420	425	430
Ser Thr Glu Trp Ala Glu Glu His Ser Arg Leu Leu Gln	Glu Arg Gly	
435	440	445
Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn	Tyr Thr Leu	
450	455	460
Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu Val Tyr	Asn Leu Thr	
465	470	475
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Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe Glu Gly Lys	Ser Leu Tyr	
485	490	495

Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro
			500				505						510		
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln
			515				520					525			
Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Lys
			530				535				540				
Thr	Asn	Lys	Val	Ser	Ser	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr
			545			550				555			560		
Tyr	Glu	Leu	Val	Val	Lys	Phe	Tyr	Asp	Pro	Thr	Phe	Lys	Tyr	His	Leu
					565			570				575			
Thr	Val	Ala	Gln	Val	Arg	Gly	Ala	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser
					580			585				590			
Ile	Val	Leu	Pro	Phe	Asp	Cys	Gln	Ser	Tyr	Ala	Val	Ala	Leu	Lys	Lys
					595			600			605				
Tyr	Ala	Asp	Thr	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met
					610			615			620				
Lys	Ala	Tyr	Met	Ile	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Asn	Asn
					625			630			635			640	
Phe	Thr	Asp	Val	Ala	Ser	Lys	Phe	Asn	Gln	Arg	Leu	Gln	Glu	Leu	Asp
					645			650			655				
Lys	Ser	Asn	Pro	Ile	Leu	Leu	Arg	Ile	Met	Asn	Asp	Gln	Leu	Met	Tyr
					660			665			670				
Leu	Glu	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Phe
					675			680			685				
Tyr	Arg	His	Thr	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly
					690			695			700				
Glu	Ser	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Ser	Ser	Lys
					705			710			715			720	
Val	Asn	Ala	Ser	Lys	Ala	Trp	Asn	Glu	Val	Lys	Arg	Gln	Ile	Ser	Ile
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Ala	Thr	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Arg	Glu	Val	Ala
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Phe	Leu	Tyr	Asn	Phe	Thr	Arg	Thr	Pro	His	Leu	Ala	Gly	Thr	Gln	Asn
					20			25			30				
aat	ttt	gag	ctt	gca	aag	caa	att	cat	gac	cag	tgg	aaa	gaa	ttt	ggc
Asn	Phe	Glu	Leu	Ala	Lys	Gln	Ile	His	Asp	Gln	Trp	Lys	Glu	Phe	Gly
					35			40			45				
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Leu	Asp	Leu	Val	Glu	Leu	Ser	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
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Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn		
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gag	att	ttc	aaa	aca	tca	tta	tct	gaa	cag	cca	ccc	cca	gga	tat	gag		288
Glu	Ile	Phe	Lys	Thr	Ser	Leu	Ser	Glu	Cin	Pro	Pro	Pro	Gly	Tyr	Glu		
85										90						95	
aat	ata	tca	gat	gtt	cca	cca	tac	agt	gcc	ttc	tct	cca	caa	ggg		336	
Asn	Ile	Ser	Asp	Val	Val	Pro	Pro	Tyr	Ser	Ala	Phe	Ser	Pro	Gln	Gly		
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aca	cca	gag	ggt	gat	cta	gtg	tat	gtc	aac	tat	gca	cga	act	gaa	gac		384
Thr	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp		
115										120						125	
ttc	ttt	aaa	ctg	gaa	cgg	gaa	atg	aag	atc	agt	tgt	tct	ggg	aag	att		432
Phe	Phe	Lys	Leu	Glu	Arg	Glu	Met	Lys	Ile	Ser	Cys	Ser	Gly	Lys	Ile		
130										135						140	
gtg	att	gcc	aga	tat	ggg	aaa	gtg	ttc	aga	gga	aat	atg	gtt	aaa	aat		480
Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn		
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Asp	Tyr	Phe	Val	Pro	Ala	Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu		
180										185						190	
cct	gga	ggt	ggt	gtc	caa	cgt	gga	aat	gtc	tta	aat	ctt	aat	ggt	gca		624
Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala		
195										200						205	
ggt	gac	ccg	ctc	aca	cca	ggt	tac	cca	gca	aat	gaa	cac	gtt	tat	agg		672
Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg		
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Ile	Gly	Tyr	Asp	Asp	Ala	Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro		
245										250						255	
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Ala	Pro	Pro	Asp	Ser	Ser	Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn		
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gtg	gga	cct	ggc	ttt	gct	gga	aac	ttt	tca	aca	caa	aag	gtc	aag	atg		864
Val	Gly	Pro	Gly	Phe	Ala	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met		
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Thr	Leu	Lys	Gly	Ala	Leu	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly		
305										310						320	
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His	Arg	Asp	Ala	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala		
325										330						335	
gct	gtt	gtt	cat	gaa	att	gtg	cgg	agc	ttt	gga	acc	ctg	aag	aag	aaa		1056
Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Lys		
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Gly	Arg	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu		
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Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu His Ser Arg	
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ctc cta caa gag cga ggt gtg gct tat att aat gct gat tct tcc ata	1200
Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile	
385 390 395 400	
gaa gga aat tac act cta aga gtt gat tgc aca cca ctg atg tac agc	1248
Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser	
405 410 415	
tta gtg tac aac cta aca aaa gag ctg caa agc cca gat gaa ggt ttt	1296
Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe	
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Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro	
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450 455 460	
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Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg	
465 470 475 480	
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Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr	
485 490 495	
cac agt gtc tat gaa aca tat gag ctg gta gta aaa ttt tat gac cca	1536
His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro	
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aca ttt aaa tac cac ctc act gtg gcc cag gtt cga gga gcg atg gta	1584
Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val	
515 520 525	
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Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr	
530 535 540	
gct gta gct ctg aag aag tat gct gac act atc tac aat att tca atg	1680
Ala Val Ala Leu Lys Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met	
545 550 555 560	
aaa cat cca caa gaa atg aag gct tac atg ata tca ttt gat tca ctg	1728
Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu	
565 570 575	
ttt tct gca gtc aat aat ttt aca gat gtt gca tct aag ttc aat cag	1776
Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln	
580 585 590	
aga ctg caa gag tta gac aaa agc aac ccc ata tta ctg aga att atg	1824
Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met	
595 600 605	
aat gac cag ctg atg tat ctg gaa cgt gca ttc att gat cct tta ggc	1872
Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly	
610 615 620	
tta cca gga agg cct ttc tac agg cat acc atc tat gct cca agc agc	1920
Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser	
625 630 635 640	
cac aac aag tat gca gga gaa tca ttc cct ggg att tat gat gcc ctt	1968
His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu	
645 650 655	
ttt gat ata agt agc aaa gtc aat gct tct aag gcc tgg aac gaa gtg	2016
Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Lys Ala Trp Asn Glu Val	
660 665 670	

aag	aga	cag	att	tct	att	gca	acc	ttt	aca	gtg	caa	gct	gca	gca	gag		2064	
Lys	Arg	Gln	Ile	Ser	Ile	Ala	Thr	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu			
																675	680	685
act	ctg	agg	gaa	gta	gct													2082
Thr	Leu	Arg	Glu	Val	Ala													
																690		

<210> 10
<211> 694
<212> PRT
<213> Mus musculus

<400> 10																			
Met	Lys	Lys	Glu	Phe	Leu	His	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys				
1					5				10						15				
Phe	Leu	Tyr	Asn	Phe	Thr	Arg	Thr	Pro	His	Leu	Ala	Gly	Thr	Gln	Asn				
					20				25						30				
Asn	Phe	Glu	Leu	Ala	Lys	Gln	Ile	His	Asp	Gln	Trp	Lys	Glu	Phe	Gly				
					35				40						45				
Leu	Asp	Leu	Val	Glu	Leu	Ser	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro				
					50				55						60				
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn				
					65				70						80				
Glu	Ile	Phe	Lys	Thr	Ser	Leu	Ser	Glu	Gln	Pro	Pro	Pro	Gly	Tyr	Glu				
					85				90						95				
Asn	Ile	Ser	Asp	Val	Val	Pro	Pro	Tyr	Ser	Ala	Phe	Ser	Pro	Gln	Gly				
					100				105						110				
Thr	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp				
					115				120						125				
Phe	Phe	Lys	Leu	Glu	Arg	Glu	Met	Lys	Ile	Ser	Cys	Ser	Gly	Lys	Ile				
					130				135						140				
Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn				
					145				150						160				
Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala				
					165				170						175				
Asp	Tyr	Phe	Val	Pro	Ala	Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu				
					180				185						190				
Pro	Gly	Gly	Val	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala					
					195				200						205				
Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg				
					210				215						220				
His	Glu	Leu	Thr	Asn	Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro				
					225				230						240				
Ile	Gly	Tyr	Asp	Asp	Ala	Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro				
					245				250						255				
Ala	Pro	Pro	Asp	Ser	Ser	Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn				
					260				265						270				
Val	Gly	Pro	Gly	Phe	Ala	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met				
					275				280						285				
His	Ile	His	Ser	Tyr	Thr	Lys	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly				
					290				295						300				
Thr	Leu	Lys	Gly	Ala	Leu	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly				
					305				310						320				
His	Arg	Asp	Ala	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala				
					325				330						335				
Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys					

340	345	350
Gly Arg Arg Pro Arg Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu		
355	360	365
Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu His Ser Arg		
370	375	380
Leu Leu Gin Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile		
385	390	395
Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser		
405	410	415
Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe		
420	425	430
Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro		
435	440	445
Glu Phe Ile Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp		
450	455	460
Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg		
465	470	475
Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr		
485	490	495
His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro		
500	505	510
Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val		
515	520	525
Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr		
530	535	540
Ala Val Ala Leu Lys Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met		
545	550	555
Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu		
565	570	575
Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln		
580	585	590
Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met		
595	600	605
Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly		
610	615	620
Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser		
625	630	635
His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu		
645	650	655
Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Lys Ala Trp Asn Glu Val		
660	665	670
Lys Arg Gln Ile Ser Ile Ala Thr Phe Thr Val Gln Ala Ala Ala Glu		
675	680	685
Thr Leu Arg Glu Val Ala		
690		

<210> 11
<211> 45
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)...(45)

<400> 11
cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 12
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 12
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 13
<211> 63
<212> DNA
<213> Clostridium tetani

<220>
<221> CDS
<222> (1)..(63)

<400> 13
ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15
gct agc cac ctg gaa 63
Ala Ser His Leu Glu
20

<210> 14
<211> 21
<212> PRT
<213> Clostridium tetani

<400> 14
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15
Ala Ser His Leu Glu
20

<210> 15
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 15
Gln Glu Arg Gly Val Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Arg Val Asp Cys Thr
20 25

<210> 16
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 16
Ala Val Val Leu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Glu Met Lys Thr Tyr
20 25

<210> 17
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 17
Met Phe Leu Glu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu His Val Ile Tyr Ala
20 25

<210> 18
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 18
Asn Ser Arg Leu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15
Val Pro Lys Val Ser Ala Ser His Leu Glu Val Asp Cys Thr Pro
20 25 30

<210> 19
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of tetanus toxoid epitope and PSM

<400> 19
Val Val Leu Arg Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15
Val Pro Lys Val Ser Ala Ser His Leu Glu Ser Phe Asp Ser Leu
20 25 30

<210> 20
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of tetanus toxoid epitope and PSM

<400> 20
Leu Met Phe Leu Glu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15
Val Pro Lys Val Ser Ala Ser His Leu Glu Pro Ser Ser His Asn
20 25 30

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial His tag

<220>
<221> CDS
<222> (1)..(18)

<400> 21 18
cat cat cat cat cat cat
His His His His His His
1 5

<210> 22
<211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial His tag

<400> 22
His His His His His His
1 5

<210> 23
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial His tag

<220>
<221> CDS
<222> (1)..(42)

<400> 23
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

42

<210> 24
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial His tag

<400> 24
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

<210> 25
<211> 69
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(69)

<400> 25

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga 48
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

gca gtc ttc gtt tcc ccc agc 69
Ala Val Phe Val Ser Pro Ser
20

<210> 26
<211> 23
<212> PRT
<213> Mus musculus

<400> 26
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly 33
1 5 10 15
Ala Val Phe Val Ser Pro Ser
20

<210> 27
<211> 33
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(33)

<400> 27
gaa caa aaa ctc atc tca gaa gag gat ctg aat 33
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 28
<211> 11
<212> PRT
<213> Homo sapiens

<400> 28
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

<210> 29
<211> 75
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(75)

<400> 29
atg aag gat tcc tgc atc act gtg atg gcc atg gcg ctg ctg tct ggg 48

Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
1 5 10 15 75
ttc ttt ttc ttc gcg ccg gcc tcg agc
Phe Phe Phe Phe Ala Pro Ala Ser Ser
20 25

<210> 30
<211> 25
<212> PRT
<213> Homo sapiens

<400> 30
Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
1 5 10 15
Phe Phe Phe Phe Ala Pro Ala Ser Ser
20 25

<210> 31
<211> 60
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(60)

<400> 31
atg aga agg atg ctt ctg cac ttg agt gtt ctg act ctc agc tgt gtc 48
Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
1 5 10 15
tgg gcc act gcc 60
Trp Ala Thr Ala
20

<210> 32
<211> 20
<212> PRT
<213> Mus musculus

<400> 32
Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
1 5 10 15
Trp Ala Thr Ala
20

<210> 33
<211> 20
<212> PRT
<213> Homo sapiens

<400> 33
Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala

1	5	10	15
Pro Asp Thr Arg			
20			

<210> 34
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Fig. 5B - Various FGF8 isoforms

<400> 34

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu			
1 5 10 15			
Val Leu Cys Leu Gln Ala Gln Glu Gly Pro Gly Arg Gly Pro Ala Leu			
20 25 30			
Gly Arg Glu Leu Ala Ser Leu Phe Arg Ala Gly Arg Glu Pro Gln Gly			
35 40 45			
Val Ser Gln Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His			
50 55 60			
Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile			
65 70 75 80			
Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val			
85 90 95			
Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe			
100 105 110			
Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val			
115 120 125			
Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys			
130 135 140			
Leu Ile Ala Lys Ser Asn Gly Lys Gly Asp Cys Val Phe Thr Glu			
145 150 155 160			
Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu			
165 170 175			
Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser			
180 185 190			
Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro			
195 200 205			
Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn			
210 215 220			
Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala			
225 230 235 240			
Pro Glu Pro Arg			

<210> 35
<211> 215
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(215)
<223> Fig. 6 - Wild Type (WT) FGF8b

<400> 35
Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10 15
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
20 25 30
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35 40 45
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50 55 60
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65 70 75 80
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85 90 95
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100 105 110
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Asp Cys Val
115 120 125
Phe Thr Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130 135 140
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145 150 155 160
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165 170 175
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180 185 190
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195 200 205
Thr Trp Ala Pro Glu Pro Arg
210 215

<210> 36
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Fig. 6 - F30N: Variant of FGF8b with P30 epitope in the N-terminal

<400> 36
Met Ala Gln Val Thr Val Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
1 5 10 15
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg Arg Leu Ile Arg
20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
50 55 60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65 70 75 80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85 90 95
Ile Ala Lys Ser Asn Gly Lys Gly Asp Cys Val Phe Thr Glu Ile
100 105 110
Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
115 120 125
Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys

130	135	140
Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg		
145	150	155
Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr		160
165	170	175
Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro		
180	185	190
Glu Pro Arg		
195		

<210> 37
<211> 208
<212> PRT
<213> Artificial Sequence

<220>
<223> Fig. 6 - F2I: Internal variant of FGF8b constructed by replacing external loops in the FGF2 structure with P2 epitope

400	37		
Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val			
1	5	10	15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg			
20	25	30	
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu			
35	40	45	
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala			
50	55	60	
Lys Leu Ile Val Glu Thr Asp Gln Tyr Ile Lys Ala Asn Ser Lys Phe			
65	70	75	80
Ile Gly Ile Thr Glu Leu Gly Ser Arg Val Arg Val Arg Gly Ala Glu			
85	90	95	
Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys			
100	105	110	
Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile Gly Leu Glu			
115	120	125	
Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met			
130	135	140	
Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln			
145	150	155	160
His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg Gly His His			
165	170	175	
Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe			
180	185	190	
Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg			
195	200	205	

<210> 38
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> Fig. 6 - F30I: Internal variant of FGF8b constructed by replacing

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external loops in the FGF2 structure with P30 epitope

<400> 38
Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1 5 10 15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
50 55 60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65 70 75 80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85 90 95
Ile Ala Lys Ser Asn Gly Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
100 105 110
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Asp Cys Val Phe Thr
115 120 125
Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr
130 135 140
Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly
145 150 155 160
Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu
165 170 175
Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu
180 185 190
Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp
195 200 205
Ala Pro Glu Pro Arg
210

<210> 39
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<223> Fig. 6 -F2C: Variant of FGF8b with P2 epitope in the C-terminal
<400> 39

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1 5 10 15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
50 55 60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65 70 75 80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85 90 95
Ile Ala Lys Ser Asn Gly Lys Gly Asp Cys Val Phe Glu Ile
100 105 110

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Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
115 120 125
Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys
130 135 140
Thr Arg Glu His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg
145 150 155 160
Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr
165 170 175
Pro Pro Phe Thr Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
180 185 190
Thr Glu Leu Pro Glu Pro Arg
195

<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> A preferred pan DR epitope (PADRE) peptide has this sequence

<400> 40

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

<210> 41

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> FGF8b specific peptide

<400> 41

Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr
1 5 10